SEQUENCE LISTING

<130>   Thomas, Susan Margaret

<120>   COMPOSITION AND METHOD FOR DETECTING MUTAGENS

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<140>   US 09/603,448
<141>   2000-06-26

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<170>   PatentIn version 3.1

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Gly Ile Ser Asp Gly Asp Leu Leu Ile Val Asp Ser Ala Ile Thr Ala
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Ser His Gly Asp Ile Val Ile Ala Ala Val Asp Gly Glu Phe Thr Val
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Ser Asn Arg Val Met Ser Thr Leu Glu Glu Leu Ser Pro Arg Val Glu
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            100   105   110

Cys Arg Asp Leu Thr Asp Phe Gly Arg Glu Ile Arg Ala Thr Val Leu
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Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
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Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Met Glu Tyr Asn
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Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
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Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
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Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
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Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
            180                 185                 190


Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser
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Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val
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gccgatgaac aaagattttc ctgtgtacta cattgacccg gataatgaga gcgttgaaat   600

ctggggagtg gttacgcatt cccttatcga gcatccggta tgtttgcgct gattgatgtc   660

aatggcatgt acgccagctg tgagcaggca tttaggccag atctggcaaa ccgagcagtg   720

gccgttttat ccaacaatga cggcaacatt gtggcccgta attacctggc gaagaaagcg   780

ggcctgaaaa tgggcgatcc gtacttcaaa gtcagaccca taatcgagcg tcataacatc   840

gctattttta gctctaatta cactctttat gcctccatgt cggcccggtt cgcggccgta   900

gttgagtccc ttgcaagcca cgtcgaacag tattcaatcg acgagctttt tgttgactgc   960

aaagggataa cggccgccat gagccttgac gctttcgggc gccaactgcg cgaggaagtc   1020

aggcgacaca caacgctggt atgcggggtc ggtattgccc gtactaagac gctggcgaag   1080

ctgtgtaacc acgctgcaaa aacatggccc gctactggcg gggtggttgc tctggacgat   1140

ggcgccagac tgaagaaatt aatgagcatc ctgccggttg cggaagtctg gggcgtcggc   1200

catcgtacag agaaagcact cgccacaatg gggatcaaaa cggtgctgga tttagccagg   1260

gcagatacgc gcctaatccg taaaacattc ggcgttgtgc ttgaaagaac ggtacgggag   1320

ttgcgcggcg aggcttgctt cagcctggaa gaaaaccctc ctgcgaagca gcagattgtt   1380

gtgtcgcgct cattcggcca acgcgtagaa accctgacgg acatgcagca ggctgtcacc   1440

12

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ggatttgcag cgcgcgcagc tgaaaaactg cgtaatgaga ggcaatactg ccgcgtcata    1500

agcgtcttta tccgtaccag tccttattca gtgcgtgata cacagtatgc caatcaggca    1560

accgaaaaac tgacggtggc aacccaggac agccgcacga taattcaggc agcacaagcc    1620

gcgctggcgc ggatctggcg ggaagatatt gcgtatgcaa aagcaggggt catgctggca    1680

gattttagcg ggaaggaggc ccagcttgat ttattcgact ctgctacgcc ttcagctggc    1740

agcgaggctt taatggctgt tcttgatggt ataaaccggc gtggaaagaa ccagcttttt    1800

tttgcaggcc agggcatcga taactccttt gccatgcgtc gtcagatgtt gtcacctgat    1860

tacacgacag actggcgctc aataccaata gccaccatca ataattacc ggcgccgtac     1920

ccgggccggt taacccctca accggccgta acaagtttcg gcacggtttc gcggttttcg    1980

gtaaaagccg tttcctctgt ataaaagatc atctaaatta tgtgtattgc acaatacata    2040

tatgtgaggt tagcagtgaa tttgcctaca cccgaaacct acgatgaact tcagagagcc    2100

tacgattttt tcaatgagaa gctattcagc aacgagctgc cgccatgcct gataacgttg    2160

cagcgtgaga agcgaacgta tggctattgt tcctttaagc gtttcgtcgg ccgtgagagt    2220

gggtacacgg tagacgagat c                                             2241
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<210> 11
<211> 146
<212> PRT
<213> Enterobacteriaceae

<400> 11

Met Lys Val Asp Ile Phe Glu Ser Ser Gly Ala Ser Arg Val His Ser
1   5   10   15

Ile Pro Phe Tyr Leu Gln Arg Ile Ser Ala Gly Phe Pro Ser Pro Ala
            20   25   30

Gln Gly Tyr Glu Lys Gln Glu Leu Asn Leu His Glu Tyr Cys Val Arg
        35   40   45

His Pro Ser Ala Thr Tyr Phe Leu Arg Val Ser Gly Ser Ser Met Glu
    50   55   60

Asp Gly Arg Ile His Asp Gly Asp Val Leu Val Val Asp Arg Ser Leu
65   70   75   80

Thr Ala Ser His Gly Ser Ile Val Val Ala Cys Ile His Asn Glu Phe
                85   90   95

13

Thr Val Lys Arg Leu Leu Leu Arg Pro Arg Pro Cys Leu Met Pro Met
        100   105   110

Asn Lys Asp Phe Pro Val Tyr Tyr Ile Asp Pro Asp Asn Glu Ser Val
        115   120   125

Glu Ile Trp Gly Val Val Thr His Ser Leu Ile Glu His Pro Val Cys
    130   135   140

Leu Arg
145

<210> 12
<211> 421
<212> PRT
<213> Enterobacteriaceae

<400> 12

Met Phe Ala Leu Ile Asp Val Asn Gly Met Tyr Ala Ser Cys Glu Gln
1   5   10   15

Ala Phe Arg Pro Asp Leu Ala Asn Arg Ala Val Ala Val Leu Ser Asn
            20   25   30

Asn Asp Gly Asn Ile Val Ala Arg Asn Tyr Leu Ala Lys Lys Ala Gly
        35   40   45

Leu Lys Met Gly Asp Pro Tyr Phe Lys Val Arg Pro Ile Ile Glu Arg
    50   55   60

His Asn Ile Ala Ile Phe Ser Ser Asn Tyr Thr Leu Tyr Ala Ser Met
65   70   75   80

Ser Ala Arg Phe Ala Ala Val Val Glu Ser Leu Ala Ser His Val Glu
            85   90   95

Gln Tyr Ser Ile Asp Glu Leu Phe Val Asp Cys Lys Gly Ile Thr Ala
            100   105   110

Ala Met Ser Leu Asp Ala Phe Gly Arg Gln Leu Arg Glu Glu Val Arg
        115   120   125

Arg His Thr Thr Leu Val Cys Gly Val Gly Ile Ala Arg Thr Lys Thr
    130   135   140

Leu Ala Lys Leu Cys Asn His Ala Ala Lys Thr Trp Pro Ala Thr Gly
14

Gly Val Val Ala Leu Asp Asp Gly Ala Arg Leu Lys Lys Leu Met Ser
              165   170   175

Ile Leu Pro Val Ala Glu Val Trp Gly Val Gly His Arg Thr Glu Lys
              180   185   190

Ala Leu Ala Thr Met Gly Ile Lys Thr Val Leu Asp Leu Ala Arg Ala
              195   200   205

Asp Thr Arg Leu Ile Arg Lys Thr Phe Gly Val Val Leu Glu Arg Thr
    210   215   220

Val Arg Glu Leu Arg Gly Glu Ala Cys Phe Ser Leu Glu Glu Asn Pro
225   230   235   240

Pro Ala Lys Gln Gln Ile Val Val Ser Arg Ser Phe Gly Gln Arg Val
              245   250   255

Glu Thr Leu Thr Asp Met Gln Gln Ala Val Thr Gly Phe Ala Ala Arg
              260   265   270

Ala Ala Glu Lys Leu Arg Asn Glu Arg Gln Tyr Cys Arg Val Ile Ser
              275   280   285

Val Phe Ile Arg Thr Ser Pro Tyr Ser Val Arg Asp Thr Gln Tyr Ala
    290   295   300

Asn Gln Ala Thr Glu Lys Leu Thr Val Ala Thr Gln Asp Ser Arg Thr
305   310   315   320

Ile Ile Gln Ala Ala Gln Ala Ala Leu Ala Arg Ile Trp Arg Glu Asp
              325   330   335

Ile Ala Tyr Ala Lys Ala Gly Val Met Leu Ala Asp Phe Ser Gly Lys
              340   345   350

Glu Ala Gln Leu Asp Leu Phe Asp Ser Ala Thr Pro Ser Ala Gly Ser
              355   360   365

Glu Ala Leu Met Ala Val Leu Asp Gly Ile Asn Arg Arg Gly Lys Asn
    370   375   380

Gln Leu Phe Phe Ala Gly Gln Gly Ile Asp Asn Ser Phe Ala Met Arg
                              15

Arg Gln Met Leu Ser Pro Asp Tyr Thr Thr Asp Trp Arg Ser Ile Pro
                405   410   415

Ile Ala Thr Ile Lys
            420

<210> 13
<211> 74
<212> PRT
<213> Enterobacteriaceae

<400> 13

Met Cys Ile Ala Gln Tyr Ile Tyr Val Arg Leu Ala Val Asn Leu Pro
1   5   10   15

Thr Pro Glu Thr Tyr Asp Glu Leu Gln Arg Ala Tyr Asp Phe Phe Asn
            20   25   30

Glu Lys Leu Phe Ser Asn Glu Leu Pro Pro Cys Leu Ile Thr Leu Gln
        35   40   45

Arg Glu Lys Arg Thr Tyr Gly Tyr Cys Ser Phe Lys Arg Phe Val Gly
    50   55   60

Arg Glu Ser Gly Tyr Thr Val Asp Glu Ile
65   70

<210> 14
<211> 1990
<212> DNA
<213> Escherichia coli

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ggacactgag aaagcagaaa gccaacaaac actatatata gcgttcgttg cagctgaag   180

cagcactaca tatagtagag aacctgtaaa acttgccaac ctgaccataa cagcgatact   240

gtataaataa acagttattt ggaagatcgc tatgaaggtc gatattttg aaagctccgg   300

cgccagccgg gtacacagca tcccttttta tctgcaaaga atttctgcgg ggttccccag   360

cccggcccag ggctatgaaa agcaggagtt aaacctgcat gagtattgtg ttcgtcaccc   420

ttcagcaact tacttcctgc gggtttctgg ctcgtcaatg gaagatggcc gcatccatga   480

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tggtgacgta ctggttgtgg atcgctcgct gacggccagc cacggctcaa tcgtagtcgc   540

ctgcatccat aatgaattta ccgtgaagcg actactgctg aggcccagac cctgcctgat   600

gccgatgaac aaagattttc ctgtgtacta cattgacccg gataatgaga gcgttgaaat   660

ctggggagtg gttacgcatt cccttatcga gcatccggta tgtttgcgct gattgatgtc   720

aatggcatgt acgccagctg tgagcaggca tttaggccag atctggcaaa ccgagcagtg   780

gccgttttat ccaacaatga cggcaacatt gtggcccgta attacctggc gaagaaagcg   840

ggcctgaaaa tgggcgatcc gtacttcaaa gtcagaccca taatcgagcg tcataacatc   900

gctatttta gctctaatta cactctttat gcctccatgt cggcccggtt cgcggccgta   960

gttgagtccc ttgcaagcca cgtcgaacag tattcaatcg acgagctttt tgttgactgc   1020

aaagggataa cggccgccat gagccttgac gctttcgggc gccaactgcg cgaggaagtc   1080

aggcgacaca caacgctggt atgcggggtc ggtattgccc gtactaagac gctggcgaag   1140

ctgtgtaacc acgctgcaaa aacatggccc gctactggcg gggtggttgc tctggacgat   1200

ggcgccagac tgaagaaatt aatgagcatc ctgccggttg cggaagtctg gggcgtcggc   1260

catcgtacag agaaagcact cgccacaatg gggatcaaaa cggtgctgga tttagccagg   1320

gcagatacgc gcctaatccg taaaacattc ggcgttgtgc ttgaaagaac ggtacgggag   1380

ttgcgcggcg aggcttgctt cagcctggaa gaaaaccctc ctgcgaagca gcagattgtt   1440

gtgtcgcgct cattcggcca acgcgtagaa accctgacgg acatgcagca ggctgtcacc   1500

ggatttgcag cgcgcgcagc tgaaaaactg cgtaatgaga ggcaatactg ccgcgtcata   1560

agcgtcttta tccgtaccag tccttattca gtgcgtgata cacagtatgc caatcaggca   1620

accgaaaaac tgacggtggc aacccaggac agccgcacga taattcaggc agcacaagcg   1680

ctggcgcgga tctggcggga agatattgcg tatgcaaaag cagggggtcat gctggcagat   1740

tttagcggga aggaggccca gcttgattta ttcgactctg ctacgccttc agctggcagc   1800

gaggctttaa tggctgttct tgatggtata aaccggcgtg gaaagaacca gcttttttttt   1860

gcaggccagg gcatcgataa ctcctttgcc atgcgtcgtc agatgttgtc acctgattac   1920

acgacagact ggcgctcaat accaatagcc accatcaaat aattaccggc gccgtacccg   1980

ggccgctcga                                                          1990
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<210>   15
<211>   146
<212>   PRT
<213>   Escherichia coli

<400>   15

17

Met Lys Val Asp Ile Phe Glu Ser Ser Gly Ala Ser Arg Val His Ser
1   5   10   15

Ile Pro Phe Tyr Leu Gln Arg Ile Ser Ala Gly Phe Pro Ser Pro Ala
            20   25   30

Gln Gly Tyr Glu Lys Gln Glu Leu Asn Leu His Glu Tyr Cys Val Arg
        35   40   45

His Pro Ser Ala Thr Tyr Phe Leu Arg Val Ser Gly Ser Ser Met Glu
    50   55   60

Asp Gly Arg Ile His Asp Gly Asp Val Leu Val Val Asp Arg Ser Leu
65   70   75   80

Thr Ala Ser His Gly Ser Ile Val Val Ala Cys Ile His Asn Glu Phe
                85   90   95

Thr Val Lys Arg Leu Leu Leu Arg Pro Arg Pro Cys Leu Met Pro Met
            100   105   110

Asn Lys Asp Phe Pro Val Tyr Tyr Ile Asp Pro Asp Asn Glu Ser Val
            115   120   125

Glu Ile Trp Gly Val Val Thr His Ser Leu Ile Glu His Pro Val Cys
    130   135   140

Leu Arg
145

<210>   16
<211>   420
<212>   PRT
<213>   Escherichia coli

<400>   16

Met Phe Ala Leu Ile Asp Val Asn Gly Met Tyr Ala Ser Cys Glu Gln
1   5   10   15

Ala Phe Arg Pro Asp Leu Ala Asn Arg Ala Val Ala Val Leu Ser Asn
            20   25   30

Asn Asp Gly Asn Ile Val Ala Arg Asn Tyr Leu Ala Lys Lys Ala Gly
        35   40   45

Leu Lys Met Gly Asp Pro Tyr Phe Lys Val Arg Pro Ile Ile Glu Arg
18

His Asn Ile Ala Ile Phe Ser Ser Asn Tyr Thr Leu Tyr Ala Ser Met
65   70   75   80

Ser Ala Arg Phe Ala Ala Val Val Glu Ser Leu Ala Ser His Val Glu
              85   90   95

Gln Tyr Ser Ile Asp Glu Leu Phe Val Asp Cys Lys Gly Ile Thr Ala
              100   105   110

Ala Met Ser Leu Asp Ala Phe Gly Arg Gln Leu Arg Glu Glu Val Arg
          115   120   125

Arg His Thr Thr Leu Val Cys Gly Val Gly Ile Ala Arg Thr Lys Thr
    130   135   140

Leu Ala Lys Leu Cys Asn His Ala Ala Lys Thr Trp Pro Ala Thr Gly
145   150   155   160

Gly Val Val Ala Leu Asp Asp Gly Ala Arg Leu Lys Lys Leu Met Ser
              165   170   175

Ile Leu Pro Val Ala Glu Val Trp Gly Val Gly His Arg Thr Glu Lys
          180   185   190

Ala Leu Ala Thr Met Gly Ile Lys Thr Val Leu Asp Leu Ala Arg Ala
          195   200   205

Asp Thr Arg Leu Ile Arg Lys Thr Phe Gly Val Val Leu Glu Arg Thr
    210   215   220

Val Arg Glu Leu Arg Gly Glu Ala Cys Phe Ser Leu Glu Glu Asn Pro
225   230   235   240

Pro Ala Lys Gln Gln Ile Val Val Ser Arg Ser Phe Gly Gln Arg Val
              245   250   255

Glu Thr Leu Thr Asp Met Gln Gln Ala Val Thr Gly Phe Ala Ala Arg
          260   265   270

Ala Ala Glu Lys Leu Arg Asn Glu Arg Gln Tyr Cys Arg Val Ile Ser
          275   280   285

Val Phe Ile Arg Thr Ser Pro Tyr Ser Val Arg Asp Thr Gln Tyr Ala

```
              290                    295                    300
```

```
Asn Gln Ala Thr Glu Lys Leu Thr Val Ala Thr Gln Asp Ser Arg Thr
305                 310                 315                 320
```

```
Ile Ile Gln Ala Ala Gln Ala Leu Ala Arg Ile Trp Arg Glu Asp Ile
                325                 330                 335
```

```
Ala Tyr Ala Lys Ala Gly Val Met Leu Ala Asp Phe Ser Gly Lys Glu
                340                 345                 350
```

```
Ala Gln Leu Asp Leu Phe Asp Ser Ala Thr Pro Ser Ala Gly Ser Glu
            355                 360                 365
```

```
Ala Leu Met Ala Val Leu Asp Gly Ile Asn Arg Arg Gly Lys Asn Gln
        370                 375                 380
```

```
Leu Phe Phe Ala Gly Gln Gly Ile Asp Asn Ser Phe Ala Met Arg Arg
385                 390                 395                 400
```

```
Gln Met Leu Ser Pro Asp Tyr Thr Thr Asp Trp Arg Ser Ile Pro Ile
                405                 410                 415
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```
Ala Thr Ile Lys
            420
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<210>  17
<211>  2574
<212>  DNA
<213>  Salmonella typhimurium

<220>
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<222>  (211)..(630)
<223>


<220>
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<222>  (633)..(1901)
<223>


<400>  17
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ccggaaaatt tacaaaaccc ataatttgaa ctgagagaga aacttacaaa cgaagcgacg   120

aagatttaaa cagtcgtagc gactccggta tcttgcgcgc atgttcaaat aacactactg   180

tatataaaaa cagtattcga ggtatggatt atg gaa ttt ttc aga cct aca gag   234
```

```
                              Met Glu Phe Phe Arg Pro Thr Glu
                              1                 5

ttg cgc gaa att att cct ctc cca ttt ttc agt tac tta gtg ccg tgt    282
Leu Arg Glu Ile Ile Pro Leu Pro Phe Phe Ser Tyr Leu Val Pro Cys
    10              15                  20

gga ttc ccc agc ccc gcg gcg gac tac att gag cag cgt atc gat ctt    330
Gly Phe Pro Ser Pro Ala Ala Asp Tyr Ile Glu Gln Arg Ile Asp Leu
25              30                  35                  40

aat gag ttg ctc gtt tct cat ccc agc tca aca tat ttt gtc aaa gcc    378
Asn Glu Leu Leu Val Ser His Pro Ser Ser Thr Tyr Phe Val Lys Ala
                45                  50                  55

tcg ggg gat tca atg att gaa gca ggc atc agc gac ggt gac ctg ctg    426
Ser Gly Asp Ser Met Ile Glu Ala Gly Ile Ser Asp Gly Asp Leu Leu
            60                  65                  70

gtg gtg gat agc tca cgg aac gct gac cac ggt gac att gta att gcg    474
Val Val Asp Ser Ser Arg Asn Ala Asp His Gly Asp Ile Val Ile Ala
        75                  80                  85

gca att gaa gga gag ttc acc gta aaa cgg ttg cag ttg cgc ccg aca    522
Ala Ile Glu Gly Glu Phe Thr Val Lys Arg Leu Gln Leu Arg Pro Thr
        90                  95                  100

gtg cag tta atc ccc atg aac ggc gcc tat cga cct ata cct gtc ggc    570
Val Gln Leu Ile Pro Met Asn Gly Ala Tyr Arg Pro Ile Pro Val Gly
105             110                 115                 120

agt gaa gac acg ctc gac ata ttc ggg gtg gtg acc ttt atc att aaa    618
Ser Glu Asp Thr Leu Asp Ile Phe Gly Val Val Thr Phe Ile Ile Lys
            125                 130                 135

gcg gtc agt tga tt atg ttc gcg ctc tgc gat gtt aat agc ttt tac    665
Ala Val Ser         Met Phe Ala Leu Cys Asp Val Asn Ser Phe Tyr
                    140                 145                 150

gcc tcc tgc gaa acg gtc ttt cgt cct gat tta tgt ggc cga ccg gtg    713
Ala Ser Cys Glu Thr Val Phe Arg Pro Asp Leu Cys Gly Arg Pro Val
                155                 160                 165

gtg gtg tta tca aac aat gat ggc tgc gtt atc gcg tgt agc gcc gag    761
Val Val Leu Ser Asn Asn Asp Gly Cys Val Ile Ala Cys Ser Ala Glu
            170                 175                 180

gcg aaa cag ctc ggt atc gca cca ggt gag cca tac ttc aaa cag aaa    809
Ala Lys Gln Leu Gly Ile Ala Pro Gly Glu Pro Tyr Phe Lys Gln Lys
            185                 190                 195

gaa cgc ttc cgg cga tcc ggt gtt gtt tgc ttc agc agt aat tac gag    857
Glu Arg Phe Arg Arg Ser Gly Val Val Cys Phe Ser Ser Asn Tyr Glu
    200                 205                 210

ctt tac gct gat atg tcg aac cgg gta atg acc aca ctc gag gag atg    905
Leu Tyr Ala Asp Met Ser Asn Arg Val Met Thr Thr Leu Glu Glu Met
215                 220                 225                 230

gtg ccg cgg gta gaa att tac agc att gat gag gcc ttt tgt gat ctg    953
```

```
      Val Pro Arg Val Glu Ile Tyr Ser Ile Asp Glu Ala Phe Cys Asp Leu
                  235             240             245

acg ggg gta cga aac tgc cgg gat ctg aca gat ttc ggg cgc gag ata    1001
Thr Gly Val Arg Asn Cys Arg Asp Leu Thr Asp Phe Gly Arg Glu Ile
            250             255             260

aga gcg acg gtc ctg aag cgc acg cac ctg act gtc ggt gta ggc att    1049
Arg Ala Thr Val Leu Lys Arg Thr His Leu Thr Val Gly Val Gly Ile
            265             270             275

gcc cag acg aaa acc ctt gcc aag ctg gct aac cat gct gcg aaa aag    1097
Ala Gln Thr Lys Thr Leu Ala Lys Leu Ala Asn His Ala Ala Lys Lys
        280             285             290

tgg cag cgc cag acc gac ggg gtg gtt gac ttg tcg aac atc gat cgc    1145
Trp Gln Arg Gln Thr Asp Gly Val Val Asp Leu Ser Asn Ile Asp Arg
295             300             305             310

cag cgt cgg ctg ctg gcc ctg ata ccc gtg gag gat gtc tgg ggt gtc    1193
Gln Arg Arg Leu Leu Ala Leu Ile Pro Val Glu Asp Val Trp Gly Val
            315             320             325

ggc agg cgc atc agt aag aag ctc aat gcc ctg ggc atc aag act gct    1241
Gly Arg Arg Ile Ser Lys Lys Leu Asn Ala Leu Gly Ile Lys Thr Ala
            330             335             340

ctc gat ctc tct gaa caa agt acc tgg atc atc agg aaa cac ttc aat    1289
Leu Asp Leu Ser Glu Gln Ser Thr Trp Ile Ile Arg Lys His Phe Asn
            345             350             355

gtc gtg ctg gag cgt acc gtg aga gag ctt cgc gga gag cca tgt ctg    1337
Val Val Leu Glu Arg Thr Val Arg Glu Leu Arg Gly Glu Pro Cys Leu
        360             365             370

gag ctc gaa gag ttt gcg ccg gca aag cag gaa atc gtt tgt agt cgc    1385
Glu Leu Glu Glu Phe Ala Pro Ala Lys Gln Glu Ile Val Cys Ser Arg
375             380             385             390

tct ttc ggc gag cgg gtc aca gac tat gag gaa atg cgc cag gct gtt    1433
Ser Phe Gly Glu Arg Val Thr Asp Tyr Glu Glu Met Arg Gln Ala Val
                395             400             405

tac agc tac gct gcg cgc gcg gca gaa aaa ctc cgc ggc gag cac cag    1481
Tyr Ser Tyr Ala Ala Arg Ala Ala Glu Lys Leu Arg Gly Glu His Gln
            410             415             420

tac tgc cgt ttc att tca aca ttc gtc aaa aca tca ccc ttt gcc ctg    1529
Tyr Cys Arg Phe Ile Ser Thr Phe Val Lys Thr Ser Pro Phe Ala Leu
            425             430             435

aac gag ccc tac tac ggt aac agc gcc gcg gtg acg ctt ctc acc ccc    1577
Asn Glu Pro Tyr Tyr Gly Asn Ser Ala Ala Val Thr Leu Leu Thr Pro
        440             445             450

acg cag gat tca cgt gac att atc aat gcg gct gtg aaa tgc ctg gat    1625
Thr Gln Asp Ser Arg Asp Ile Ile Asn Ala Ala Val Lys Cys Leu Asp
455             460             465             470

aaa ata tgg cgc gac ggc cat cgc tac cag aaa gcg ggg gtg atg ctg    1673
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22

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      Lys Ile Trp Arg Asp Gly His Arg Tyr Gln Lys Ala Gly Val Met Leu
                 475                 480                 485

      ggt gac ttc ttc agt cag ggc gta gcg caa ctc aac ctt ttc gac gat    1721
      Gly Asp Phe Phe Ser Gln Gly Val Ala Gln Leu Asn Leu Phe Asp Asp
                 490                 495                 500

      aac gcg ccg cgc gcc ggt agt gcg aag ttg atg gaa gta ctg gac cat    1769
      Asn Ala Pro Arg Ala Gly Ser Ala Lys Leu Met Glu Val Leu Asp His
                 505                 510                 515

      ctt aac gca aaa gac ggg aag ggg acg ctg tac ttc gcc ggg cag ggg    1817
      Leu Asn Ala Lys Asp Gly Lys Gly Thr Leu Tyr Phe Ala Gly Gln Gly
                 520                 525                 530

      atg tcg caa cag tgg gct atg aag cga gaa atg ctt tcg cct cgg tac    1865
      Met Ser Gln Gln Trp Ala Met Lys Arg Glu Met Leu Ser Pro Arg Tyr
      535                 540                 545                 550

      acc aca aga tac tct gat cta ctg cgt gtt aag taa cttgtgcgat         1911
      Thr Thr Arg Tyr Ser Asp Leu Leu Arg Val Lys
                 555                 560

      caatgcctga gatggttgcc aaatcatccc cgttctctaa ccggttttgg tcgcacaaga  1971

      tcacaggaac ctctcacgat gagcttgtgc gatcaatgcc tgagatggtt gccaaatcat  2031

      ccccgttctc taaccggttt tggtcgcaca agatcacagg aacctctcac gatgaggcgc  2091

      atgtatcctg gtttacgaca tcagaaaatg tggcgcgttt attgcccggc aggcgttgtg  2151

      agacgtcact tatttacgcc aggtttcagc cgtagcgaca ggcatgaata aaaagagtat  2211

      ggcaatcagc gtgataatgc taaaaaacaa ttaatatttt tttaacaaaa ctaaagcttg  2271

      ctatgttcag ttaaccatgc gttaatggtt gtgcggtttg atacaaactt atctgaagta  2331

      gtgattgtaa tatttctcat catttgttcc tcttgagatc tcctttaggt ttttttctct  2391

      ctgataattt tcttcaggcc attttccgca agggctcatt cgaaaggtaa caatattatg  2451

      acgacgaaaa tcactggttt agtaaaatgg tttaaccctg aaaagggctt tggtttcatt  2511

      acgcctaaag atggcagcaa agatgtgttt gtgcattttt cagccattca aagtaatgaa  2571

      ttc                                                               2574


      <210>    18
      <211>    139
      <212>    PRT
      <213>    Salmonella typhimurium

      <400>    18

      Met Glu Phe Phe Arg Pro Thr Glu Leu Arg Glu Ile Ile Pro Leu Pro
      1               5                   10                  15


      Phe Phe Ser Tyr Leu Val Pro Cys Gly Phe Pro Ser Pro Ala Ala Asp
                                     23
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Tyr Ile Glu Gln Arg Ile Asp Leu Asn Glu Leu Leu Val Ser His Pro
          35   40   45

Ser Ser Thr Tyr Phe Val Lys Ala Ser Gly Asp Ser Met Ile Glu Ala
     50   55   60

Gly Ile Ser Asp Gly Asp Leu Leu Val Val Asp Ser Ser Arg Asn Ala
65   70   75   80

Asp His Gly Asp Ile Val Ile Ala Ala Ile Glu Gly Glu Phe Thr Val
               85   90   95

Lys Arg Leu Gln Leu Arg Pro Thr Val Gln Leu Ile Pro Met Asn Gly
          100   105   110

Ala Tyr Arg Pro Ile Pro Val Gly Ser Glu Asp Thr Leu Asp Ile Phe
          115   120   125

Gly Val Val Thr Phe Ile Ile Lys Ala Val Ser
     130   135

<210> 19
<211> 422
<212> PRT
<213> Salmonella typhimurium

<400> 19

Met Phe Ala Leu Cys Asp Val Asn Ser Phe Tyr Ala Ser Cys Glu Thr
1   5   10   15

Val Phe Arg Pro Asp Leu Cys Gly Arg Pro Val Val Val Leu Ser Asn
          20   25   30

Asn Asp Gly Cys Val Ile Ala Cys Ser Ala Glu Ala Lys Gln Leu Gly
          35   40   45

Ile Ala Pro Gly Glu Pro Tyr Phe Lys Gln Lys Glu Arg Phe Arg Arg
     50   55   60

Ser Gly Val Val Cys Phe Ser Ser Asn Tyr Glu Leu Tyr Ala Asp Met
65   70   75   80

Ser Asn Arg Val Met Thr Thr Leu Glu Glu Met Val Pro Arg Val Glu
               85   90   95

24

Ile Tyr Ser Ile Asp Glu Ala Phe Cys Asp Leu Thr Gly Val Arg Asn
            100   105   110

Cys Arg Asp Leu Thr Asp Phe Gly Arg Glu Ile Arg Ala Thr Val Leu
            115   120   125

Lys Arg Thr His Leu Thr Val Gly Val Gly Ile Ala Gln Thr Lys Thr
        130   135   140

Leu Ala Lys Leu Ala Asn His Ala Ala Lys Lys Trp Gln Arg Gln Thr
145   150   155   160

Asp Gly Val Val Asp Leu Ser Asn Ile Asp Arg Gln Arg Arg Leu Leu
                165   170   175

Ala Leu Ile Pro Val Glu Asp Val Trp Gly Val Gly Arg Arg Ile Ser
            180   185   190

Lys Lys Leu Asn Ala Leu Gly Ile Lys Thr Ala Leu Asp Leu Ser Glu
        195   200   205

Gln Ser Thr Trp Ile Ile Arg Lys His Phe Asn Val Val Leu Glu Arg
    210   215   220

Thr Val Arg Glu Leu Arg Gly Glu Pro Cys Leu Glu Leu Glu Glu Phe
225   230   235   240

Ala Pro Ala Lys Gln Glu Ile Val Cys Ser Arg Ser Phe Gly Glu Arg
                245   250   255

Val Thr Asp Tyr Glu Glu Met Arg Gln Ala Val Tyr Ser Tyr Ala Ala
            260   265   270

Arg Ala Ala Glu Lys Leu Arg Gly Glu His Gln Tyr Cys Arg Phe Ile
        275   280   285

Ser Thr Phe Val Lys Thr Ser Pro Phe Ala Leu Asn Glu Pro Tyr Tyr
    290   295   300

Gly Asn Ser Ala Ala Val Thr Leu Leu Thr Pro Thr Gln Asp Ser Arg
305   310   315   320

Asp Ile Ile Asn Ala Ala Val Lys Cys Leu Asp Lys Ile Trp Arg Asp
                325   330   335

25

Gly His Arg Tyr Gln Lys Ala Gly Val Met Leu Gly Asp Phe Phe Ser
        340   345   350

Gln Gly Val Ala Gln Leu Asn Leu Phe Asp Asp Asn Ala Pro Arg Ala
        355   360   365

Gly Ser Ala Lys Leu Met Glu Val Leu Asp His Leu Asn Ala Lys Asp
        370   375   380

Gly Lys Gly Thr Leu Tyr Phe Ala Gly Gln Gly Met Ser Gln Gln Trp
385   390   395   400

Ala Met Lys Arg Glu Met Leu Ser Pro Arg Tyr Thr Thr Arg Tyr Ser
                405   410   415

Asp Leu Leu Arg Val Lys
                420

<210> 20
<211> 2138
<212> DNA
<213> Salmonella typhimurium

<400> 20
gatatccaaa ctgaccccaa aagggtaggg ggagaatgtc ccttgccgat aaaactgttc   60

ccggtttgtt atttctctgc ccgctgttaa aagttgaaag ttgataactt tgcagtaaaa   120

tgccgttatc atatatactg tataaatgta cagctaagga gaggcattaa tgtcactaaa   180

acctatgaaa tcagcccctg acaccaaaga aactatccct ttctttggcg agctcgtacc   240

cgcaggtttc cctagccctg ctgctgggtg ggaagaggct gaacttaatc ttcatacgct   300

ggtggttact catccagcca gcacgtactt cttgcgcgtg acaggtgact ccatgcagga   360

tgctcggata cattctggtg acgtgctggt ggttgatcgc tcagaaactc cagagcaggg   420

tagtattgtt gttgccagca tcgacaacga atttacagtc aagaaactca tcttgcggcc   480

acgtccatgc cttatgccga tgaacccggc atacccacct atctattttg accctgaaag   540

taacgacgtt gaaatttggg gtgtggtgac ttactcatta atgaagcaca aaaaatgtat   600

ggcctgatcg acattaattc ctgctactgt gcctgcgagc aagcattcag gcccgatctt   660

gctggtaaac ccgtagtagt tttgtcaaac aatgatgcca gctgcatagc ccgtaacaag   720

caggcgaaag cccttggtat aaaaatgggc gagccattct ttaaaatcaa agatctcata   780

gaacggaaca atgtcgctgt tttcagttca aactatgccc tttattccgc atttagttcc   840

26

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cggttttgcat ctgttataga gtcactgact ccgcgtagct cagtgtattc aatcgatgaa      900

ctttggtttg atgccacgaa tatcactggt ttaatgactc ttgatgccta tggccgcatg      960

ttgcgagaag aggtacagcg tcagacaacg cttacttgtg gtgttgggat agcaccgaca     1020

aaaacactcg cgaaattgtg ttctcatgct tcaaaaacct atccggcaac tggcggagtt     1080

gtcgcgcttg atgatgttac ccgtttagaa aagctgatgc ggcttgtgcc cgttgaagac     1140

gtgtggggtg ttggcccacg gctgggtaaa aggcttcggt ttatgggagt ggaaaccgcg     1200

tttcaactat cctgccttga tcctgttcgg gtacgaaagc agttcaatgt tgtccttgag     1260

cgtaccgtca gggaactccg gggggagcct tgcatggcgc ttgacgaaaa tgatgtgatg     1320

aaacagcaaa tagtcgtttc ccgctccttc ggtgagcgag tcaccaacct tcatgaaatg     1380

cagcaagcca taaccgatta tgcggctcgc gctgccgaaa aactccggca agaaaaaggg     1440

tatgtctctg taattggtgt ttttatacgc accagcccct acgcagtaaa tgatgtacct     1500

tattccaatc aggctactga aatgctggtg actccctcca cgacagcag ggatattatt      1560

aatgctgcac aacgcgcatt aacggatctg gaggccagaa gtccgttatg ctaaagcagg     1620

tgtgatgctt tgtgatattc gcgagcgtga gcctcaactt gatttgttca ctgaatcggc     1680

ccagtaccgc aacagtgaaa atctcatgca attactggat actctcaaca agcagggtag     1740

acacaatttg tttttttgccg gacaaggtat aaaccccgtt ttcgcaatga agagaaatat     1800

gctatcccct gcatatttga ctaggctggg atgatttacc aaaggttagg ttaggataag     1860

cccactaacc atcaaaaaga cataattttt ccttggtgtt tcacttcgcc cccctcactc     1920

gtccggcagc gcaatttggt tctcaaggtt acgtgttcaa aaacagctat aagattatgg     1980

tcacgcgctg taagccatgc cagaactaaa taaattggat tttttcgtaa tgaaaatata     2040

gcgacgaacg ttgcaaaact gtttttattgc tacaattccc cttgttggct aaaatacata     2100

ctgtataaac tgacaggggt atccgctatg gatttaaa                             2138
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<210> 21
<211> 145
<212> PRT
<213> Salmonella typhimurium

<400> 21

Met Ser Leu Lys Pro Met Lys Ser Ala Pro Asp Thr Lys Glu Thr Ile
1   5   10   15

Pro Phe Phe Gly Glu Leu Val Pro Ala Gly Phe Pro Ser Pro Ala Ala
            20   25   30

Gly Trp Glu Glu Ala Glu Leu Asn Leu His Thr Leu Val Val Thr His
        35   40   45

Pro Ala Ser Thr Tyr Phe Leu Arg Val Thr Gly Asp Ser Met Gln Asp
    50   55   60

Ala Arg Ile His Ser Gly Asp Val Leu Val Val Asp Arg Ser Glu Thr
65   70   75   80

Pro Glu Gln Gly Ser Ile Val Val Ala Ser Ile Asp Asn Glu Phe Thr
                85   90   95

Val Lys Lys Leu Ile Leu Arg Pro Arg Pro Cys Leu Met Pro Met Asn
            100   105   110

Pro Ala Tyr Pro Pro Ile Tyr Phe Asp Pro Glu Ser Asn Asp Val Glu
        115   120   125

Ile Trp Gly Val Val Thr Tyr Ser Leu Met Lys His Lys Lys Cys Met
    130   135   140

Ala
145

<210> 22
<211> 339
<212> PRT
<213> Salmonella typhimurium

<400> 22

Met Tyr Gly Leu Ile Asp Ile Asn Ser Cys Tyr Cys Ala Cys Glu Gln
1   5   10   15

Ala Phe Arg Pro Asp Leu Ala Gly Lys Pro Val Val Val Leu Ser Asn
            20   25   30

Asn Asp Ala Ser Cys Ile Ala Arg Asn Lys Gln Ala Lys Ala Leu Gly
        35   40   45

Ile Lys Met Gly Glu Pro Phe Phe Lys Ile Lys Asp Leu Ile Glu Arg
    50   55   60

Asn Asn Val Ala Val Phe Ser Ser Asn Tyr Ala Leu Tyr Ser Ala Phe
65   70   75   80

Ser Ser Arg Phe Ala Ser Val Ile Glu Ser Leu Thr Pro Arg Ser Ser
28

Val Tyr Ser Ile Asp Glu Leu Trp Phe Asp Ala Thr Asn Ile Thr Gly
            100   105   110

Leu Met Thr Leu Asp Ala Tyr Gly Arg Met Leu Arg Glu Glu Val Gln
            115   120   125

Arg Gln Thr Thr Leu Thr Cys Gly Val Gly Ile Ala Pro Thr Lys Thr
            130   135   140

Leu Ala Lys Leu Cys Ser His Ala Ser Lys Thr Tyr Pro Ala Thr Gly
145   150   155   160

Gly Val Val Ala Leu Asp Asp Val Thr Arg Leu Glu Lys Leu Met Arg
                165   170   175

Leu Val Pro Val Glu Asp Val Trp Gly Val Gly Pro Arg Leu Gly Lys
            180   185   190

Arg Leu Arg Phe Met Gly Val Glu Thr Ala Phe Gln Leu Ser Cys Leu
            195   200   205

Asp Pro Val Arg Val Arg Lys Gln Phe Asn Val Val Leu Glu Arg Thr
210   215   220

Val Arg Glu Leu Arg Gly Glu Pro Cys Met Ala Leu Asp Glu Asn Asp
225   230   235   240

Val Met Lys Gln Gln Ile Val Val Ser Arg Ser Phe Gly Glu Arg Val
            245   250   255

Thr Asn Leu His Glu Met Gln Gln Ala Ile Thr Asp Tyr Ala Ala Arg
            260   265   270

Ala Ala Glu Lys Leu Arg Gln Glu Lys Gly Tyr Val Ser Val Ile Gly
        275   280   285

Val Phe Ile Arg Thr Ser Pro Tyr Ala Val Asn Asp Val Pro Tyr Ser
    290   295   300

Asn Gln Ala Thr Glu Met Leu Val Thr Pro Ser Asn Asp Ser Arg Asp
305   310   315   320

Ile Ile Asn Ala Ala Gln Arg Ala Leu Thr Asp Leu Glu Ala Arg Ser

Pro Leu Cys

<210> 23
<211> 736
<212> DNA
<213> Aequorea victoria

<220>
<221> CDS
<222> (14)..(730)
<223>

<400> 23
aagctttatt aaa atg tct aaa ggt gaa gaa tta ttc act ggt gtt gtc   49
            Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val
            1   5   10

cca att ttg gtt gaa tta gat ggt gat gtt aat ggt cac aaa ttt tct   97
Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser
        15   20   25

gtc tcc ggt gaa ggt gaa ggt gat gct act tac ggt aaa ttg acc tta   145
Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu
        30   35   40

aaa ttt att tgt act act ggt aaa ttg cca gtt cca tgg cca acc tta   193
Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu
45   50   55   60

gtc act act ttc ggt tat ggt gtt caa tgt ttt gct aga tac cca gat   241
Val Thr Thr Phe Gly Tyr Gly Val Gln Cys Phe Ala Arg Tyr Pro Asp
                65   70   75

cat atg aaa caa cat gac ttt ttc aag tct gcc atg cca gaa ggt tat   289
His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr
                80   85   90

gtt caa gaa aga act att ttt ttc aaa gat gac ggt aac tac aag acc   337
Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr
        95   100   105

aga gct gaa gtc aag ttt gaa ggt gat acc tta gtt aat aga atc gaa   385
Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu
        110   115   120

tta aaa ggt att gat ttt aaa gaa gat ggt aac att tta ggt cac aaa   433
Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys
125   130   135   140

ttg gaa tac aac tat aac tct cac aat gtt tac atc atg gct gac aaa   481
Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys
                    145   150   155

caa aag aat ggt atc aaa gtt aac ttc aaa att aga cac aac att gaa   529

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Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu
            160                 165                 170

gat ggt tct gtt caa tta gct gac cat tat caa caa aat act cca att      577
Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile
            175                 180                 185

ggt gat ggt cca gtc ttg tta cca gac aac cat tac tta tcc act caa      625
Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln
            190                 195                 200

tct gcc tta tcc aaa gat cca aac gaa aag aga gac cac atg gtc ttg      673
Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu
205                 210                 215                 220

tta gaa ttt gtt act gct gct ggt att acc cat ggt atg gat gaa ttg      721
Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu
                225                 230                 235

tac aaa taa ctgcag                                                    736
Tyr Lys



<210>  24
<211>  238
<212>  PRT
<213>  Aequorea victoria

<400>  24

Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1               5                   10                  15


Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
            20                  25                  30


Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
            35                  40                  45


Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
    50                  55                  60


Gly Tyr Gly Val Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Gln
65                  70                  75                  80


His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85                  90                  95


Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
                100                 105                 110


Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
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            115                    120                      125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
    130                 135                 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145                 150                 155                 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
                165                 170                 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
                180                 185                 190

Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser
            195                 200                 205

Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val
    210                 215                 220

Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys
225                 230                 235
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